Studies on the transcriptional regulation in a toxic cyanobacterium Microcystis aeruginosa(Digest_要約)

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Summary

Forecasting of *Microcystis* bloom occurrence and termination is an important issue for water quality management throughout the world. However, how environmental factors (e.g., nutrient supply, light and temperature) effect on the dynamics of cyanobacterial blooms have not been elucidated. Therefore, none of strategy which perfectly and definitively forecast the toxic cyanobacterial blooms is available. Alternatively, I attempted to identify genes related with bloom formation and termination of *Microcystis* to predict its blooms by monitoring those genes. Therefore, I investigated *Microcystis* gene expression during phage infection, because phage infection is estimated to be major cause of death in natural environment. For the prediction of bloom formation, I searched for a gene maker of normally growing *Microcystis*, checkpoint factor which coordinates chromosome replication and cell division throughout the transcriptional regulation of major cell division gene, *ftsZ*.

In Chapter 2, I revealed that stress response genes involved in protection of photosystem II (PSII) are highly transcribed during phage infection. In addition, alternative sigma factor, *sigB*, which induced under various stress condition and may regulates transcription of some of stress response genes, was highly induced. These suggest that phage infection directly or indirectly induces protection of PSII via transcriptional regulation of stress response genes, and this regulation, at least partially, may be mediated by SigB.

In Chapter 3, I explored DNA binding protein bond to upstream sequence of *ftsZ* using electrophoresis mobility shift assay (EMSA), and showed that the DNA binding protein was the bacterial universal repressor LexA. To estimate regulatory system, the

recognition sequence GTWCN$_7$GTWC determined by EMSA using mutant probes were scanned on the whole *Microcystis* genome. This analysis revealed that *Microcystis* LexA regulon does not contain classical SOS genes. When compared with predicted LexA regulon among four cyanobacterial species, the regulon composition was different among each organism. In addition, *ftsZ* was found only in *Microcystis*. These data support the idea that cyanobacterial LexA regulons are diversified within the phyla and thus, bring fitness advantage for inhabitant in various environments. Considering that *Microcystis* lives in the water surface floating with gas vesicle, this organism frequently exposed to oxidized condition (i.e. UV, photooxidation and oxygen supersaturation) than non-floating cyanobacteria. Therefore, coordination of chromosome replication and cell division via transcriptional regulation of *ftsZ*, which is meditated by DNA damage-inducible LexA, may be beneficial to arrest sterile division sequence when DNA is damaged.